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(19) Eur pâisches Patentamt
Eur pean Patent Office
Office européen des brevets



(11) Publication numb r:

0 679 716 A1

(12)

EUROPEAN PATENT APPLICATION
published in accordance with Art.
158(3) EPC

(21) Application number: 95900295.7

(51) Int. Cl.: C12N 15/11, C12Q 1/68,
//G01N33/566

(22) Date of filing: 11.11.94

(26) International application number:
PCT/JP94/01916

(27) International publication number:
WO 95/14772 (01.06.95 95/23)

(30) Priority: 12.11.93 JP 355504/93

(43) Date of publication of application:
02.11.95 Bulletin 95/44

(84) Designated Contracting States:
AT BE CH DE DK ES FR GB GR IE IT LI LU MC
NL PT SE

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(54) GENE SIGNATURE.

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomoly or discriminating cells. The cloned gene can produce portein utilized as a medicine or the like.

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Table 1

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AG	AI	AK	AM	AS	AU	AY	BA	BC	BE	BF	BG	BH	BI	BK
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
95	00106	00094	8	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
96	00107	00095	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
97	00108	00096	31	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
98	00109	00097	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
99	00110	00098	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
100	00111	00099	38	7	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
101	00112	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
102	00114	00101	38	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
103	00115	00102	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
104	00116	00103	17	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
105	00117	00104	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
106	00118	00105	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
108	00120	00107	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
109	00121	00108	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
110	00122	00109	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
111	00123	00110	14	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
112	00124	00111	6	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
113	00125	00112	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
114	00127	00113	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
115	00128	00114	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
116	00129	00115	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
117	00130	00116	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
118	00131	00117	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
119	00132	00118	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
120	00133	00119	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
121	00134	00120	24	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
122	00135	00121	81	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
123	00136	00122	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
124	00137	00123	16	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
125	00138	00124	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
126	00139	00125	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
127	00140	00126	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
128	00141	00127	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
129	00142	00128	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

Table 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:

- (A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
- (B) STREET: 41-8, Takada 3-chrome, Toshima-ku
- (C) CITY: Tokyo
- 10 (E) COUNTRY: JAPAN
- (F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

15 (iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
- (B) COMPUTER: IBM PC compatible
- 20 (C) OPERATING SYSTEM: PC-DOS/ MS-DOS
- (D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

- (A) APPLICATION NUMBER: EP 95900295.7

25 (vi) PRIOR APPLICATION DATA

- (A) APPLICATION NUMBER: PCT/JP94/01916
- (B) FILING DATE: 11. November 1994

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SEQ ID NO:111
 SEQUENCE LENGTH:375
 SEQUENCE TYPE:nucleic acid
 5 TOPOLOGY:linear
 CLONE:HUMGS00124

SEQUENCE DESCRIPTION:
 GATCCTACCT ATCAAGCACT AAAAAGTTGA ACCATTATAAC TTTATATCTG TAATGATACT 60
 10 GATTATGAAA TGTCCCCCTCA AACTCATTGC AGCAGATAAC TTTTTGAGT CATTGACTTC 120
 ATTATATATT TAAAAAAATTG TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180
 ATAATGCTTT GGAANAATGG GTCTTTATA GGAAAAAACC TGGGATAACT GATTTCTATG 240
 15 GCTTCAAAG CTNAAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTT 300
 ACTGTCAGNT TAANTTACAG CTTTATGGG TGGTTAACCTT TTGTCNCATT TTCAAAAAAN 360
 CCNGGGNNNN NNNNN 375

SEQ ID NO:112
 SEQUENCE LENGTH:356
 20 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00125

SEQUENCE DESCRIPTION:
 GATCTCTGTT TTGTTGTTGA AAATTCACTT GTATACTTTT GTTTTNATCT AGGACTTCAT 60
 25 GTTTTTNAAGCAGCTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120
 AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180
 TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTTGTATAC TTTCCCTTTT CAAATTATAG 240
 30 TTTATCTNCT GTATAACTGA TTTATAAAGG TTTTGTAACA TTNTNAATA CTCATTGTCA 300
 ATTGAGAAA AAGGACATAT GAGTTTTNC ATTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113
 SEQUENCE LENGTH:351
 35 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS00127

SEQUENCE DESCRIPTION:
 GATCACATTA TNATAAATAA ATGAAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60
 40 GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTA CTCTGCCTCA CCAAACACAT 120
 GCTAGGATAT AACCCCCAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180
 TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240
 TTCTGTAATT GAGAAAATGT TCACCAAATN ATACTTTTA GTGATTACA TGTACATTTT 300
 45 ATAGGGACA TGTTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114
 SEQUENCE LENGTH:352
 SEQUENCE TYPE:nucleic acid
 50 TOPOLOGY:linear
 CLONE:HUMGS00128

5 SEQ ID NO:7844
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

10 SEQ ID NO:7845
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTCGCTCGCC CATGTATAGG GACAGCATT CTGAGAG 37

15 SEQ ID NO:7846
SEQUENCE LENGTH:38
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

20 SEQ ID NO:7847
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CCAGGGTTTT CCCAGTCACG AC 22

25 SEQ ID NO:7848
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
TCACACAGGA AACAGCTATG AC 22

50 Claims

- 55 1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
10
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
15
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
20
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
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Fig. 1

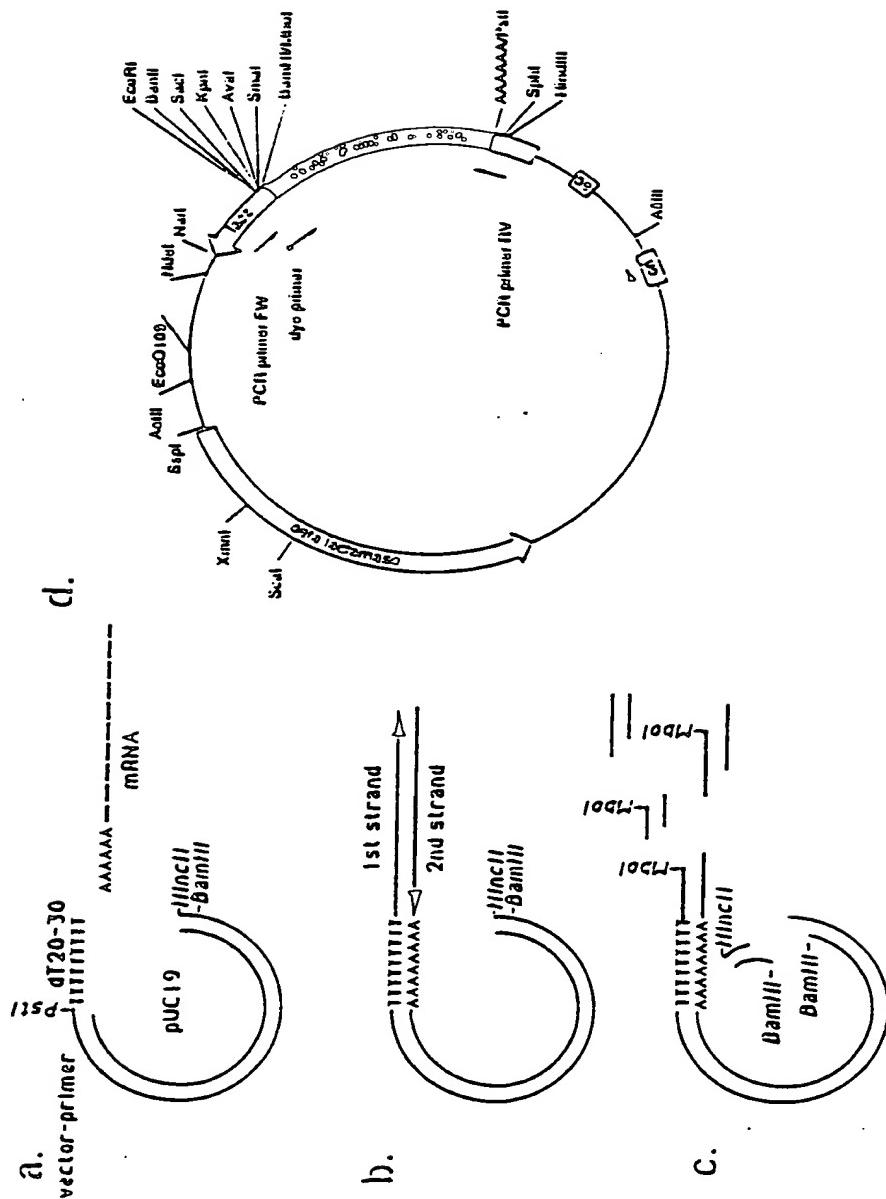


Fig. 2

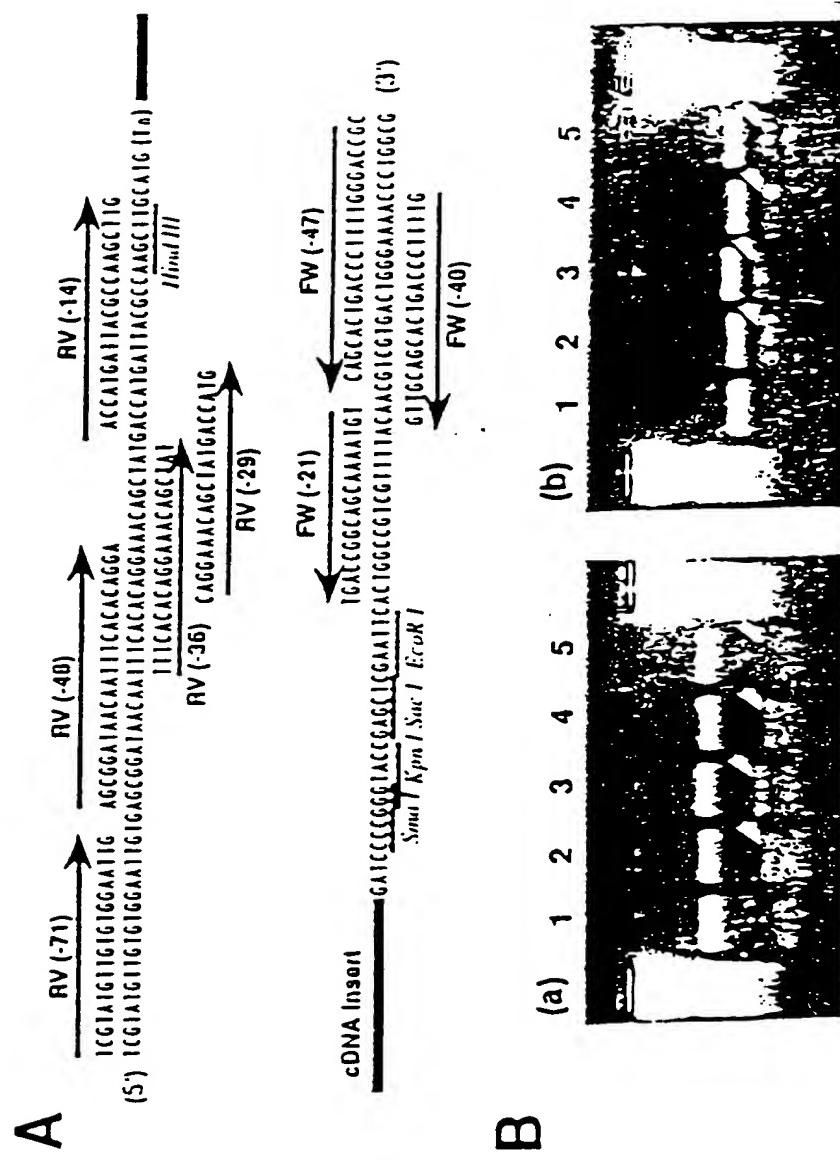


Fig. 3

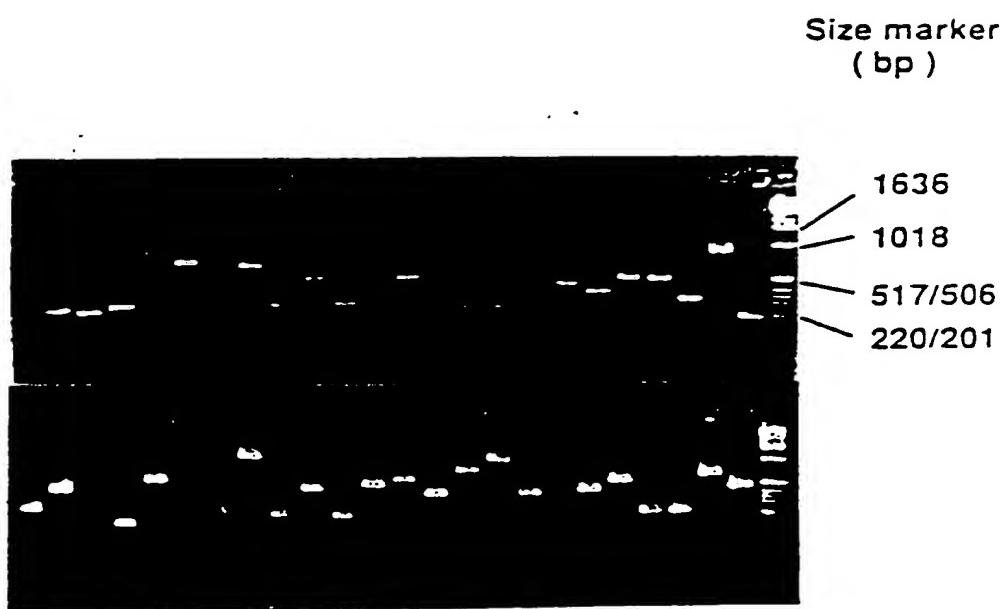


Fig. 4

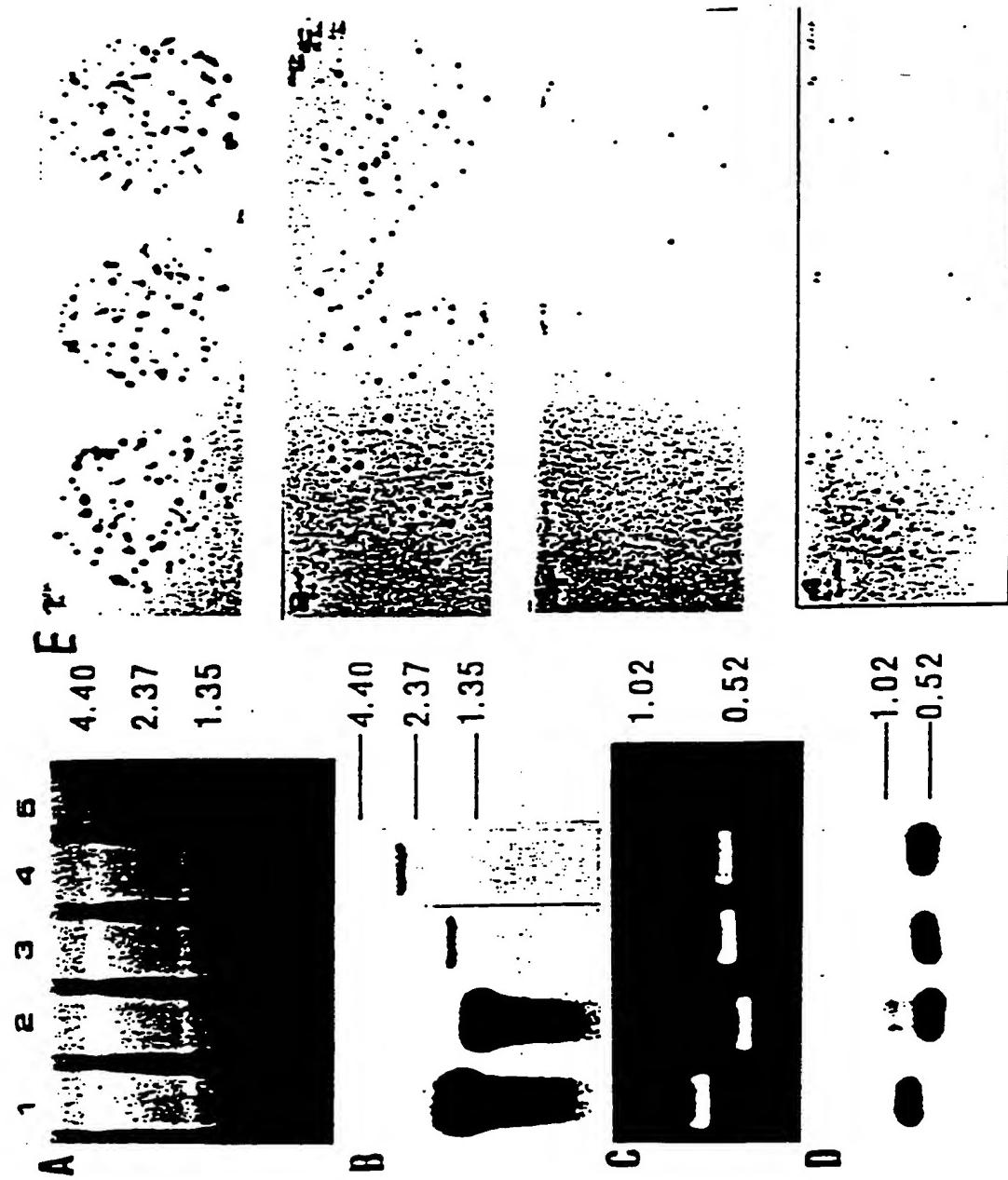


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1-c	α 1-antitrypsin	HnRNP core protein A1	Inter- α -tryptsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b)x10	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A In 902 (%)	B "In 0,800 (%)"	C "In 26,400 (%)"
I	a15	Elongation factor - 1 α	22 (2.2)	307 (3.5)	NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT
	lb030	α -1-antitrypsin	0 (0.0)	119 (1.4)	NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT
	c13a04	NADP (II) Menadione oxidoreductase	4 (0.4)	27 (0.3)	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT
	s155	unknown	1	2	5 (0.02)
	s159	unknown	1	2	4 (0.02)
	s639	unknown	1	1	3 (0.01)
	s635	unknown	1	0	2 (0.01)
II	s170	unknown	1	0	1 (0.004)
	s151	unknown	1	0	1 (0.004)
	s167	unknown	1	0	1 (0.004)
	s615	unknown	1	0	1 (0.004)
	s617	unknown	1	0	0 (<0.004)
	s632	unknown	0	0	0 (<0.004)

Fig. 6

GS	CII	Chromosomal position	Sense	Antisense		AT	T1O	HE	HO	CO	G	I
				Antisense	Antisense							
g1601038	pm1256		CAGAGCCCCAGTACACAT	AAGTTATGTTGGGGCTTAG	48	114	115	110	-	-	-	2
g1601076	pm1244		AATGGGAAGGTACACTGA	CCACATTCCTGACTTGAGA	48	83	81	>200	>200	-	-	-
g1601073	pm1063		TGAACTTGGGATACCTATCT	ACAGTAACCCGAAAGGCT	48	124	103	107	-	-	-	-
g1601087	pm1172		GTCACITCAAGCCATAGCAC	ACCACITCAAGCCACAT	50	104	104	100	>200	6	6	6
g1601094	pm0347		GCCCTAACCGAGGAAC	TAATTCACCTGGTAAAC	51	114	116	>200	200	-	-	-
g1601116	pm1171		GGGTTTCAATAGGTAGACC	GCCCCAACTGCAAACAO	49	95	95	76	107	-	-	-
g1601191	pm0609		TTGGCTATTGTTAACTTGT	GGCIGAACATCCTCTTG	47	97	97	-	>200	-	-	-
g1601200	pm1151		TTAGGAAACCCATTGGGAGCC	AATATCTGGGTTAGTCAC	47	97	98	-	-	-	-	-
g1601216	pm0902		TCAGGTCTGCTGGAGAAG	AACACAGCACAGTATG	53	120	122	>200	>200	-	-	-
g1601166	pm1518		AAAGTGTACAGATAATTGAGA	TGCATAACCACTCTCAT	47	110	125	>200	>200	-	-	-
g1601164	pm1120		CCAAAAGACTCTGGAAACA	TTGGGAGGCCATAGACAG	51	100	100	>200	-	-	-	-
g1601168	pm0927		TACTCACTGGAAAGTAAAC	CAGGGACCACTTCTTCA	40	98	98	-	-	2	2	2
g16011521	pm1195		CCCATAATCAATTTGTTAAAG	TTGAAATCAGAGACATGAACT	43	102.1/5	100	>200	>200	-	-	-
g1601154	pm1291		CCAGAGAGTCAGGGATG	GGTACAAAGTGCAAAGACT	46	57	57	78	155	-	-	-
g1601152	pm1206	1	CCACATGTCCTCTGACTG	AAACCTTATGGGCTCTCT	44	58	58	>200	>200	-	-	-
g1601150	pm1150	2	CAAGATACCTCTGATGATA	AAACAGTAGTCCTGGAGAT	46	81	109	-	-	-	-	-
g16011520	pm1170	2	AGGTGAAATGGGCTCTCT	CCCGTTATGGCTACAGCT	48	119	119	93	115	-	-	-
g16011658	pm0321	2	AAAGCAATACAAATACAA	TTCATACTGTTAACAGIA	40	90	90	-	-	-	-	-
g16011041	pm0925	2	TAAGTACAGCTAGTATAG	TAAGTAAATAGCTGGTAA	45	68	68	-	-	-	-	-
g16011050	pm1210	2	CCAGATGGAAAGGAAGCT	CTGGATAAGGAAATCAAAG	47	125	125	150	>200	-	-	-
g1601211	pm1159	2	TCAGGTCTTGTCTTAAAT	GGAAATATGGCTCTGTTG	43	103	103	-	-	-	-	-
g1601252	pm0935	2	AGGCCCTCTGGCTCTCAT	TATGCTCAGTCGGCTTATG	52	137	137	>200	-	-	-	-
g1601293	pm1268	2	TTTGTCACGTACGTAAGTACT	AICCTGCTCACTATAGTA	45	105	108	-	-	-	-	2
g16011438	pm1235	2	TTTATGGGAGCTTATCTG	AGTCCTCATCTCTCACATG	45	67	65	>200	>200	-	-	2
g1601142	pm1161	2	TTCGTTCCGGCTCTAAGT	ATGTCATTTGGTAATGAGG	45	75	75	170	190	-	-	-
g1601143	pm1245	2	ATTCACGTGTTGTAAGG	ACTGATTGTTGGCCACCTG	44	68	67	-	-	-	-	-
g16011335	pm1246	2	CGAACATTCACCTCTATA	ATGATTATTTAGGAGAA	43	63	63	-	-	-	-	2
g1600813	pm0449	3	TCIGGCCTTGGGGTGGGA	GGCCCACTGAGTACAGTC	51	115	115	-	-	-	-	6
g1601001	pm1158	3	AAAGAAACGACACTGCTAA	ATGTTAGACAAATGCAAG	42	90	90	-	-	-	-	-
g1601218	pm1234	3	GTAGTCCTGCTGGCTTGG	AGGGATTTGATTCCTACAT	43	77	77	-	-	-	-	-
g1601219	pm0668	3	GGTCCTGTTTATTGACAT	AAACAGAGGATGTCAGA	43	75	75	155	>200	-	-	-
g1601277	pm1129	3	GATCCCTGGGGTAGTCAGTC	CIGGAAATAACGGGAACT	46	81	81	160	140	-	-	-
g1601206	pm1032	3	ACCCAGTCCTCAATTCGAT	ACACCTCCCAGGCTTACI	55	105	105	113	>200	-	-	-
g1601118	pm1209	3	ATCAGGGCTGGCTAGTAT	TTAAGAGATGAAATTAGT	42	130	130	>200	>200	-	-	-
g1601165	pm1255	3	GTCCTTGGCTCTATGTTGTA	AGGCAATTATTTGACGTTA	43	90	90	95	>200	-	-	3
g1601271	pm1152	3										

Fig. 7

91000444	pm1236	GACCAAGTTCTCTCATAT	GTCAGTTTATGAGAGA	42	62	>200	69
91001052	pm1151	GTGCCATACACTGTTAT	GTCATATTCATCATCA	4	4	80	60
91001215	pm0988	AGAAATTATAGATTAAGGT	TAGATCAAGTGGCTGTG	4	4	100	130
91001294	pm1267	ATCAAGTTATGCTCA	CATCCATACATACAGTC	4	4	116	180
91000991	pm0990	TCTGGTAGAGGAGACACAA	TCAAGGAGAACAGCATC	5	5	>200	100
91000594	pm1009	AAGCAAGCTTACACAG	CTAAGGAGCTGACCTCAT	5	5	102	200
91001065	pm0119	TCACCGAGTATTACAGT	GAGACATAAGCTGAAT	5	5	87	>200
91001101	pm2264	TTACCTTACCGGTTCTAC	AGACAAATACCAAAGGC	5	5	120	200
91001161	pm1160	ATTGGAGTGTTTACIA	ADATAGGAGCTTATTC	5	5	93	100
91000051	pm2220	AATGCACTAGTCCTTCA	CTAACCTCTMAGCTCTCT	5	5	99	>200
91001226	pm1154	CATGAGCACGACAAACAG	CCTGGCTCTCTCTGAGA	6	6	78	72
91001224	pm1216	TAGGEAACACGAGAAGG	AGGAGCTGCTGAGGTC	6	6	104	145
91001457	pm1785	TATATGCAATATTCCAAAGTCG	TCTATATTCGGCTCTTAATC	6	6	65	110
91001523	pm0205	TIGTAACCTGTCTCTCTA	TTTAAAGCTGTTAAAT	6	6	>200	90
91001525	pm0228	GCACCTAAGCTCCAAAGT	TTTATACAGCTCAGGC	6	6	>200	100
91001562	pm1269	TCTGGCAITGACAGGACCAC	TTGGAGTTATAGTCATTC	6	6	>200	100
91000221	pm0991	GACCTGAATGTGATGATG	ACTTACCTTATGGGAAATT	7	7	>200	45
91001145	pm0281	-AGCCAACCTGGGTCACT	CCACGGACAGTGAGTCAT	7	7	>200	2
91001169	pm0219	AATCATTTGGCAGACIGTA	AGAACACTTACAGACA	7	7	70	>200
91001179	pm1101	TCAAGCAGCTGCTCAGATA	TTTCAGGTTATACGTTTA	7	7	69	120
91001227	pm0956	AACAGATATGGCTGTCAGACT	TCCATTATAGGCCAGTCCTAG	6	6	76	170
91001176	pm1252	TIGCTCTATGGCTCTAC	AAAACCAAAACACACTAAG	9	9	81	105
91001248	pm1208	TGTAATGATTTGGATCTIC	CAAAAGCAAAAGCAGATA	9	9	93	115
91000260	pm0995	TIGECATCAAACACATACA	CITTCAGTTGGTTGTTCTG	9	9	95	85
91001055	pm0959	TTAAAGGATACCCATATG	CACAGCTTATGGAACT	9	9	55	55
91001157	pm0547	AAGTATGCTGCAAGTGTAA	AGAAAACACTCTCTGIGG	9	9	74	72
91001264	pm1235	TGTGAAATCTATCTCTCT	CCACCTGTCATATCATG	9	9	133	200
91000224	pm1266	ATCAAACACACATACAGA	ACTATATATACCTGCACT	10	10	100	200
91001169	pm0890	GAATAGCTGGAGATTCAC	GGGAGATCATACCTICAGCA	10	10	121	134
91001215	pm0445	AAAGTACCTGAGGAGCTGAA	AGGAAACACTCTCTGAGCT	10	10	64	95
91001232	pm0293	AGGGTAAGGGTATTCTACG	GTCACCTGTTGAGGACTA	10	10	153	>200
91001469	pm0539	AACCTCTAGTAAAGCTG	TTATTAACCAACCTGAA	10	10	65	-
91001570	pm2810	CIGTAAGGTTGGATATGT	TCATCTTCTACCACTTATT	11	11	47	47
91000223	pm0266	AGTGTATGGAAAGCTCTG	CTTCATGAGCTGATAGC	12	12	75.02	75
91001163	pm2256	TCTCCATATCACACAGT	ATGATTCGAGGAACTGAG	12	12	130	103
91001193	pm1193	CACACATAAAGAACATA	ACCCATTAATTGTTCTCAC	12	12	69	>200
91001235	pm2290	CATCATGGTACATCAGAG	CAGTTGTCACATGTTATG	12	12	100	120
91001274	pm1355	AGATGTCAGTATCTCTCTG	DAGACAGGGAAAGGACAC	12	12	82	91
91001208	pm0268	CCAAGTGTAGGGTACAG	TICATGACCTGGTTAC	12	12	95	200
91000153	pm2615	CTAGATTTAAAGCGATTC	AGTATGCTAAGGAGAGA	12	12	104	>200

Fig. 8

91001011	13	pm1659	TGTAAGCCATACAGACTA	AGACAGACTATGGCACTA
91001290	13	pm1721	GCGCTTCATGGCTGGGT	GCAGTATCATGGCTATCCTC
91001282	13	pm0110	ACTGAATGGACATAGCT	TACATACAGACATGIGA
91001366	13	pm2164	TGCTAGCTTCCCCCTA	GAGCATTCCTGGTCTCTA
91001269	13	pm2301	CATGAACCTGCTCACGAA	GCCTACTTATGCTGAC
91001492	13	pm0541	AAATGAAATGAAATGCACT	ATTTAGTTACAGGAGAT
91001367	13	pm0441	GTTTAGTTGGATTTGGG	CATTCCACTCTTACATTCT
91001364	14	pm2307	CGTTCCTAACCTGAAATC	AATGCTCATTTATCTCAAG
91001376	14	pm2019	ATCACAAATTCTTAGTG	ACGAAACATTTGGAGAT
91001229	14	pm0220	TCCCCTCCAGTGAAGT	TGAGAACAAAAGACCAGT
91000980	15	pm0985	TGGAAATGGAACTCTGCTA	ACTATGCTGGCTGAAATGG
91001242	16	pm1127	CCCTTGTTTACATGCTCA	TATTAAATCTTCCATTCT
91001516	16	pm1541	ACAGTGCTAAATCAAGGIG	TCTGACACTCAAGTGCTAT
91001566	16	pm0913	TTGGTCGGACTATGTAAT	TCACCTTATGGAACTCAG
91000806	16	pm1157	CCTCTTACGTTCTACAG	TAGAGGAGAACCTGGTT
91001015	17	pm1269	ATATTCACCTTCCCTTCAAT	TCATAATGCTCCTCAGG
91001156	17	pm0202	CAGAAATTAAATGCGCAAAT	TGTATCTGGCCTTATG
91001171	17	pm2117	AAAATCTTGGTTTATTC	GTGATGCTACTGACATTC
91001301	17	pm01026	TAATTTGGAAATCTCTGGA	ACACATTTGGCTGCTTAACT
91001316	17	pm0511	TGTCACAGCAGCTCTCAT	TCGACATTTTATCCACC
91001326	17	pm0520	CATCTCACAGAACAAAC	ACCTAAAGCCTCAGAAC
91001193	17	pm02212	TCACCTGAAATAGGTTGT	GAACATACCGTTTATTCI
91001322	17	pm0642	GTCTTACGACATTCAGT	ACTTCCTCTGGKUGACACA
91001074	18	pm1015	TGTCCTTCAGCTTGTAG	GTCATCTGGCTTGTCTAG
91001117	19	pm0289	GGATACACCAAGCTGCTG	GCAGGTTAAACAGATIA
91001167	19	pm1666	GAAGGCCACCCGACCTCA	GGAGGATTTGGGAACGGT
91001069	20	pm1079	GGCATGGCTGAAAGTGT	TTAAGGAGCTTACCTGGATA
91001048	20	pm1116	GCCTTACGGATCTGCCTC	ACCCCTAACCTAACCTAG
91001069	20	pm0112	TGCTGGAGTACTCTACAG	TCCTCTATGGCTGCTGTT
91001128	20	pm0222	CIGCTGGCTACTCTACTC	CAATGCTCTAGAGGACAT
91001122	20	pm0647	TCTGAAAGATGAAACACA	ATCTTATCCAAACGGAGT
91001158	20	pm1774	GGAGGCCACATGGATGATG	AAAGTGTACCTGACAGT
91001210	20	pm01235	AGCCATCTGGTTATGCTTA	GGATGCTCCCTCTCTGTC
91001277	20	pm0701	TCCAGGGGGTAAAGCCAG	AGAAGGCCAAAGTACCTC
91001295	21	pm2101	GTCAGCTCATGCTACAG	TTTATGCTGACACAGAT
91001227	21	pm0516	CTTCCTCTTAAAGTAGAG	ACATTTGGCTTAAATGAA
91002374	22	pm0912	GGTTAGTTGTTACCTTATG	AGTGTGACCCCTCTCTGTC
91001444	22	pm0911	GGCTCTCTCTCCCACTGT	AGAAGGCCAAAGTACCTC
91001773	22	pm1231	TGAGCTGGCTACCTGAG	AAACAGGGTGGTGGTTTC
91002228	22	pm1228	TACAGGCCCTCCAGCTAAC	TTTATCTGGCACTACAA

Fig. 9

91000999		X	CTACCATAGTACCGATT	TACCCACCACTATTAGCA
91001119	p1n2180	X	GGAGGGAGATAATATTGT	AAAAAAATCCGAAAGACIA
91001161	p1n0508	X	TCTTAATGIGACCAAGTT	GGAGGTATGAGATAACAT
91001406	p1n1294	X	TAATGCCGTGATGTCGTA	GTAAGGTATACCTGTCATGA
91001166	p1n2289	1..10	ATCCGTGAAATACCTG	GGGGAGAGACATCACATGC
91001176	p1n0111	1..2,12,13Y	ATCCGTGAGGATGTAAT	AATACAAAGCTAACACCAA
91001401	p1n2222	1..2,3,5..12,14,17..X	TGGGATGACATCTCAT	TTTATGTAACAAAGCACT
910003601	p1n0314	1..2,6..X	TATCAAGCTGAAATGTCAC	TTACGAAATCCGAAACEA
91000140	p1n1461	1..3,4,5..16	TCCAATGAGAAGGTTA	ATTTGACACCAGTGAG
91001151	p1n1561	2..20,21,22	GTCTGTCAGGCAAGATCA	TTTTATGGTGCTCCAAAGI
91000336	p1n2295	2..4..5,10,12,15..17,20,21..Y	GACCTGTACATCTGGACT	TATATGGTGTACACTGG
91000177	p1n0913	2..5,14..C	GCCTGTTATTCACCACTC	AICICCCCTTGCTCCAGTTA
91001192	p1n1853	2..9,12	TCTGGACATCCAGACAG	CAGTCAAACCAACAGGTAT
91000213	p1n1770	2..9,13,17..X	TGCAATAMGGGAAGACCA	CGTGTAGGTGGTGAATAG
91000919	p1n0885	20..X	GTCAITTTGATGCAATTCC	ACATTITTTATTTCAAGG
91001169	p1n0157	2..10,13	CATGIACTGAGGCACTC	CAACTACAAACCCAACT
91000071	p1n2651	2..14..H	CAGGGACGGAGCAGGAAG	CAATTAAACCAATGGAGG
91001126	p1n2632	2..6	TTGGGAAATAAGTTAGACAG	ATAGTATGGGTGACACAGA
91001391	p1n1113	2..8	TGGATTTGTTACCTGTIT	ACACCTTCAGGAGTGTAC
91000677	p1n2250	3..9,10,15	GGACATACAGGCAACATCA	CTCTTAAACCAACAGGAG
91000603	p1n0626	4..6	GGATTTCATTCGCTCAT	CTTTATGAGGCTTAC
91001212	p1n1234	6..20	GGATTAAAGGAAACATA	CGTCGAGGCGGATAAAC
91001112	p1n0506	7..10	AGATGCTAACATAGGTG	TTTATGACATACAGGAGT
91001111	p1n1353	9..11	CCAGACTACAGGTGATGCC	CCCTTACCCGAAACICIT
91001353	p1n0115	9..1..A1	ACCAGTCACGCTGTTAAATA	CCCCATAAAGGAAAGGAACTIC
91001261	p1n01224	10..15..22	AGAAAATGTTACTGCTAT	4..12..15..3
91001154	p1n2120	10..15..22	ACTACCCCTAAATATAGTT	10..5
91000230	p1n2003	11..A1	ATACCACTTCGGCTTCAGG	11..10..5
91000314	p1n2613	12..19	GCACCMAGGAGGACTTCAG	11..20..5
91001101	p1n2273	12..A1	GAICCACTGCTCGTTTAT	12..25..5
91001401	p1n2225	13..16	ATCTGIGGIGGCTCTCC	12..20..5
91002294	p1n2280	14..16	AACCGTTTACCCATCT	13..15..5
91001435	p1n1683	17..20..C	TGTGGTTACCATGAGAC	14..20..5
91001191	p1n1740	17..22..Y	GAATGTCATCCGAGCTG	14..8..1
91000516	p1n0564	17..C	TTTATCCCAGGACAGAC	16..6..2
91001169	p1n2217	17..C	ACTTAAAGTAGCTTGTACG	19..120..120..5
91001140	p1n1213	18..C	CCCCAGTAAAGATATGT	14..95..95..5
91001217	p1n1116	19..20	TGCAAGTGATTTCAGAG	16..7..2..5
91001089	p1n2924	19..22	ATCCCTGCTAACACATCAC	16..110..110..5
91001172	p1n0887	19..22	GCCGTCATCIGGAAACAACT	14..9..8..5

Fig. 10

Fig. 11

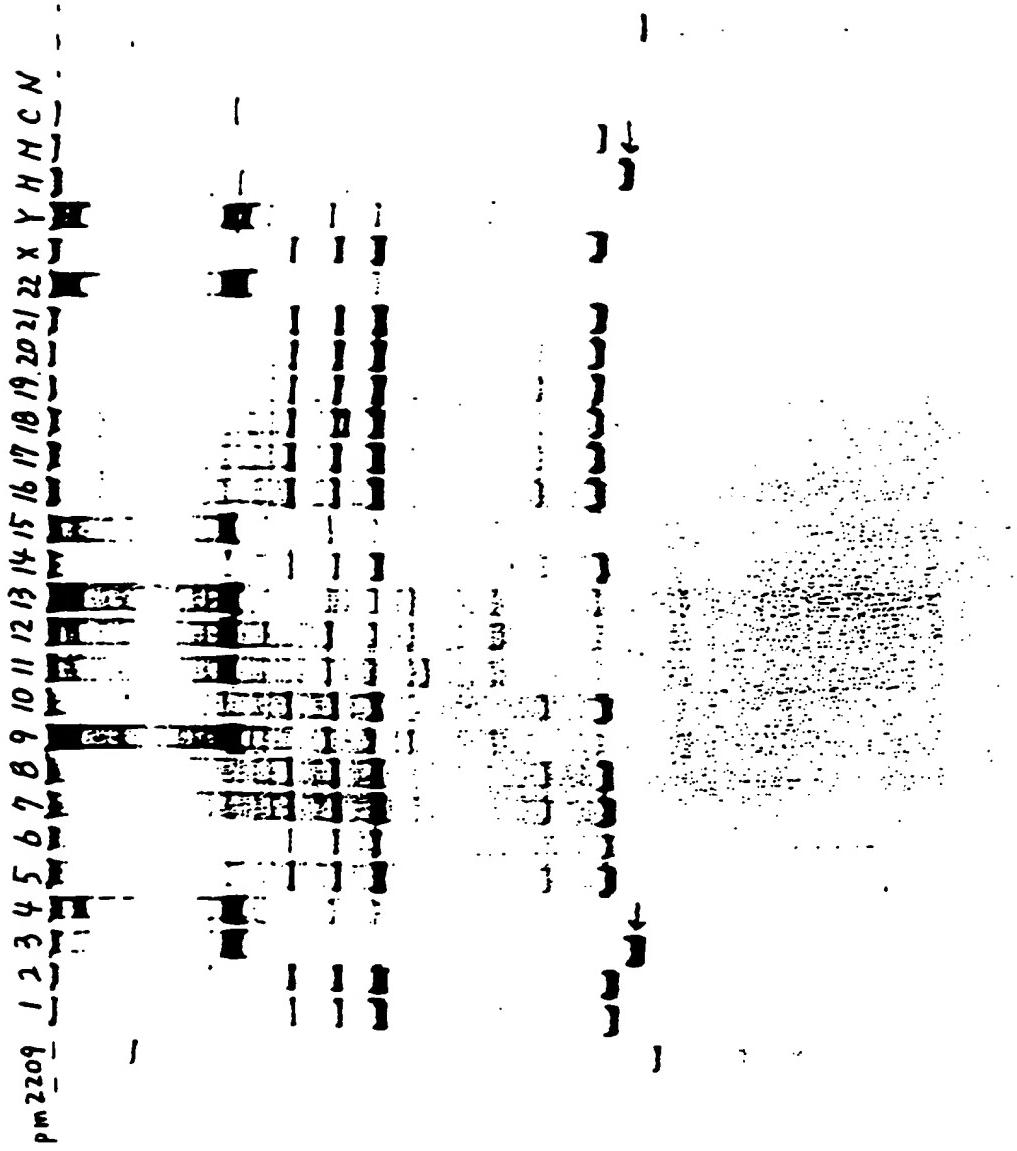


Fig. 12

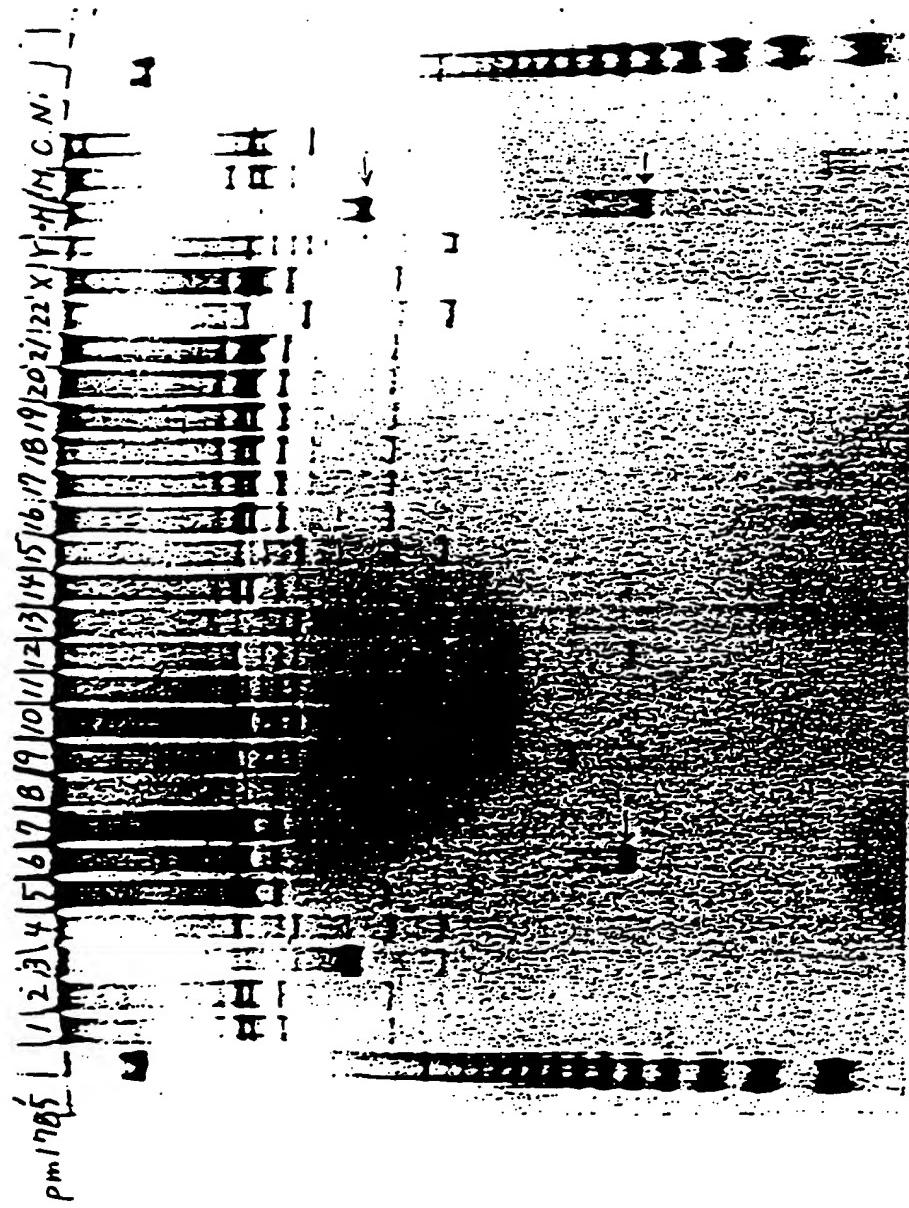


Fig. 13

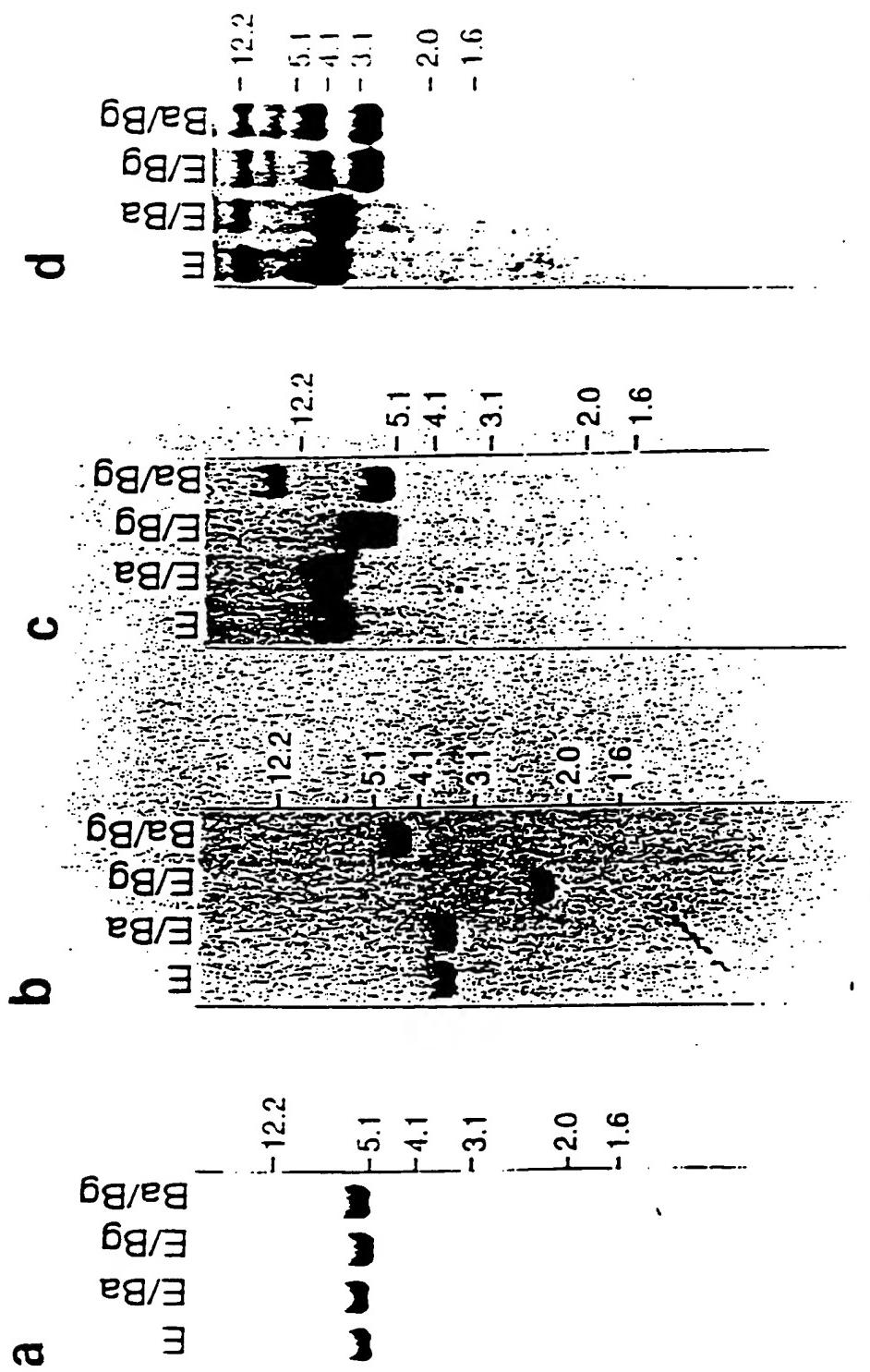


Fig. 14

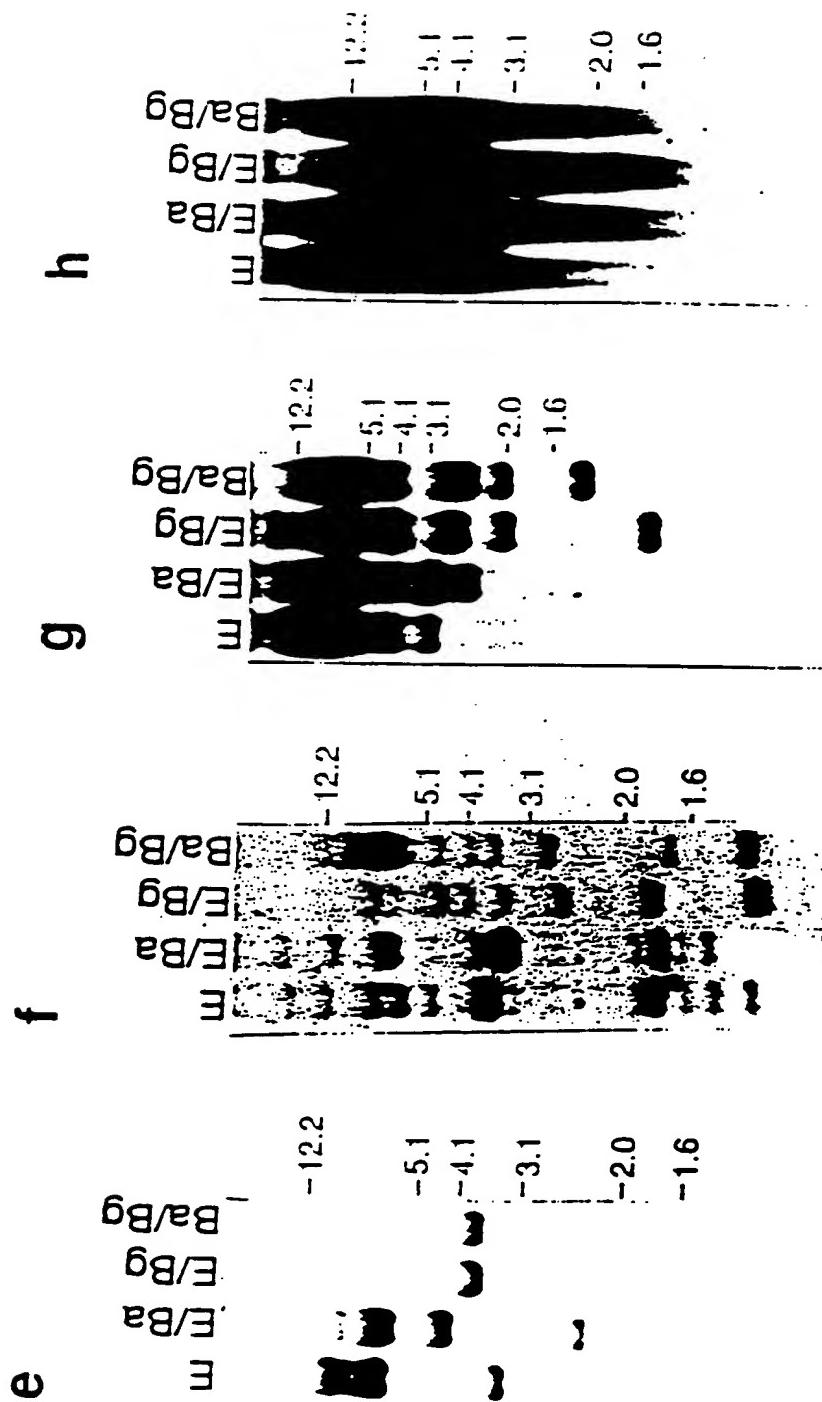


Fig. 15

Hybrid cells used for Southern hybridization

Hybrid cell . chromosome No.	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	95 (8)	0
GM10253	5	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A *	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868 *	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	L76	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11416 *	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10496	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	95 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

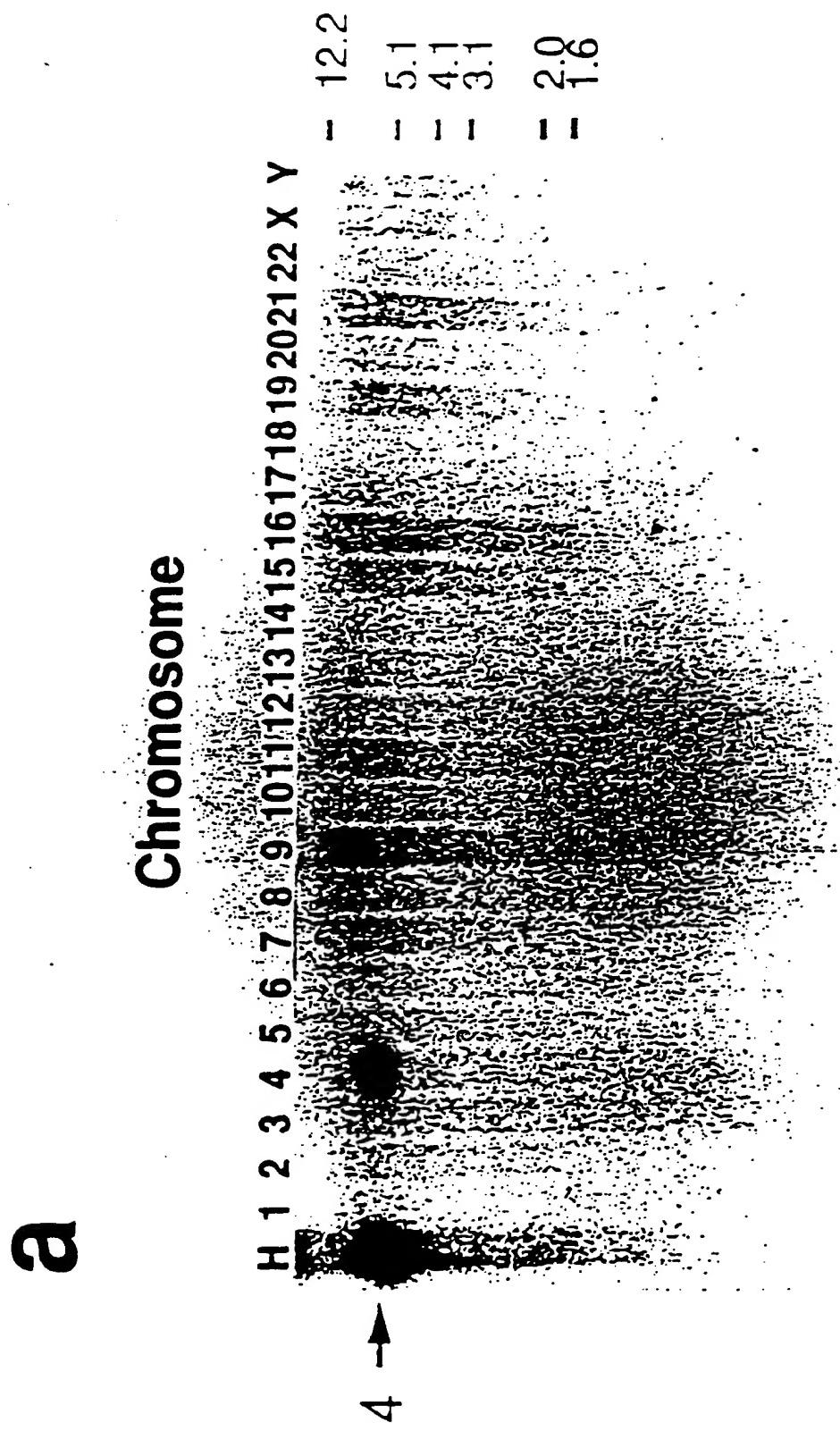
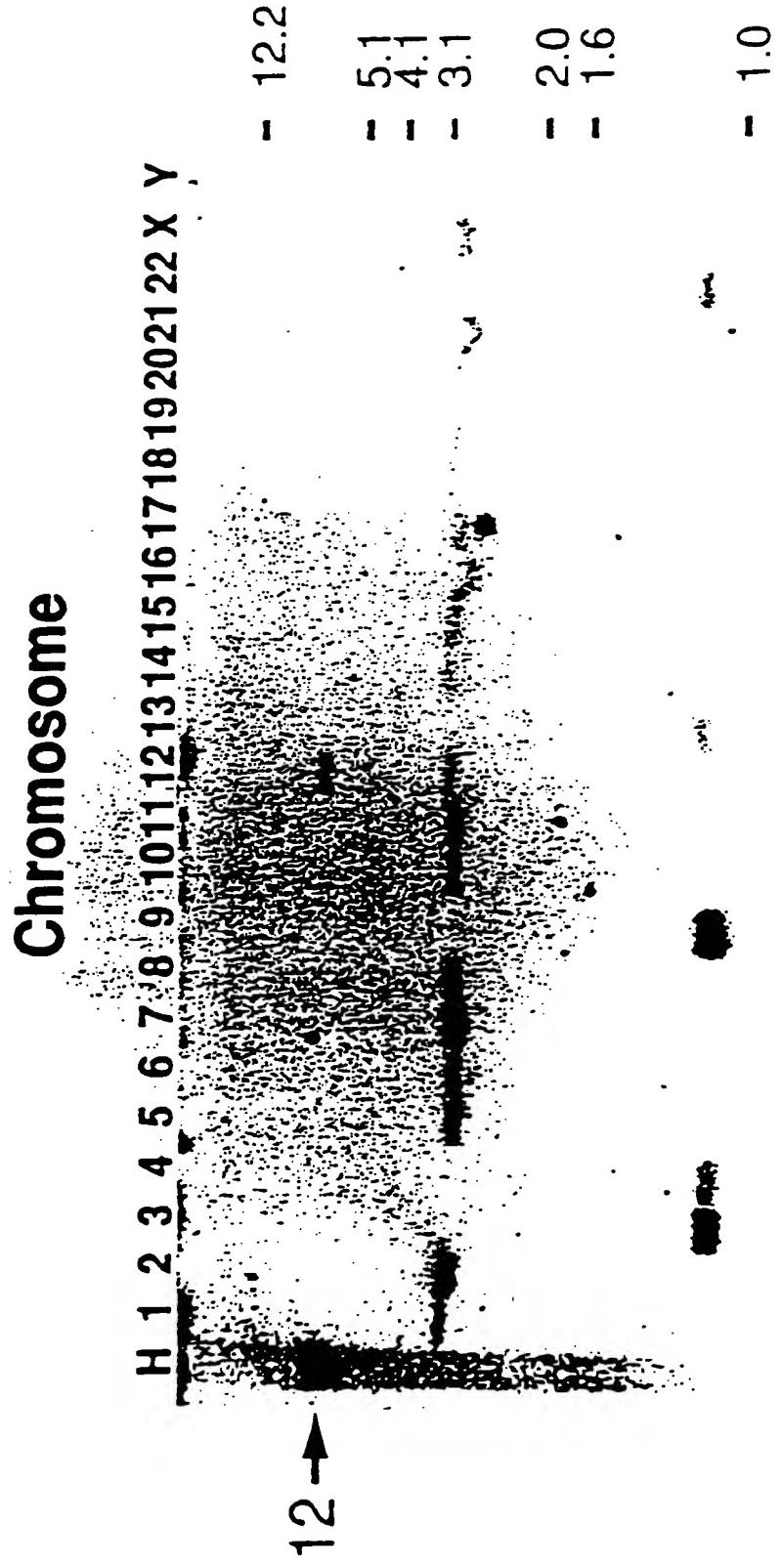


Fig. 17

b



C

Chromosome

H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

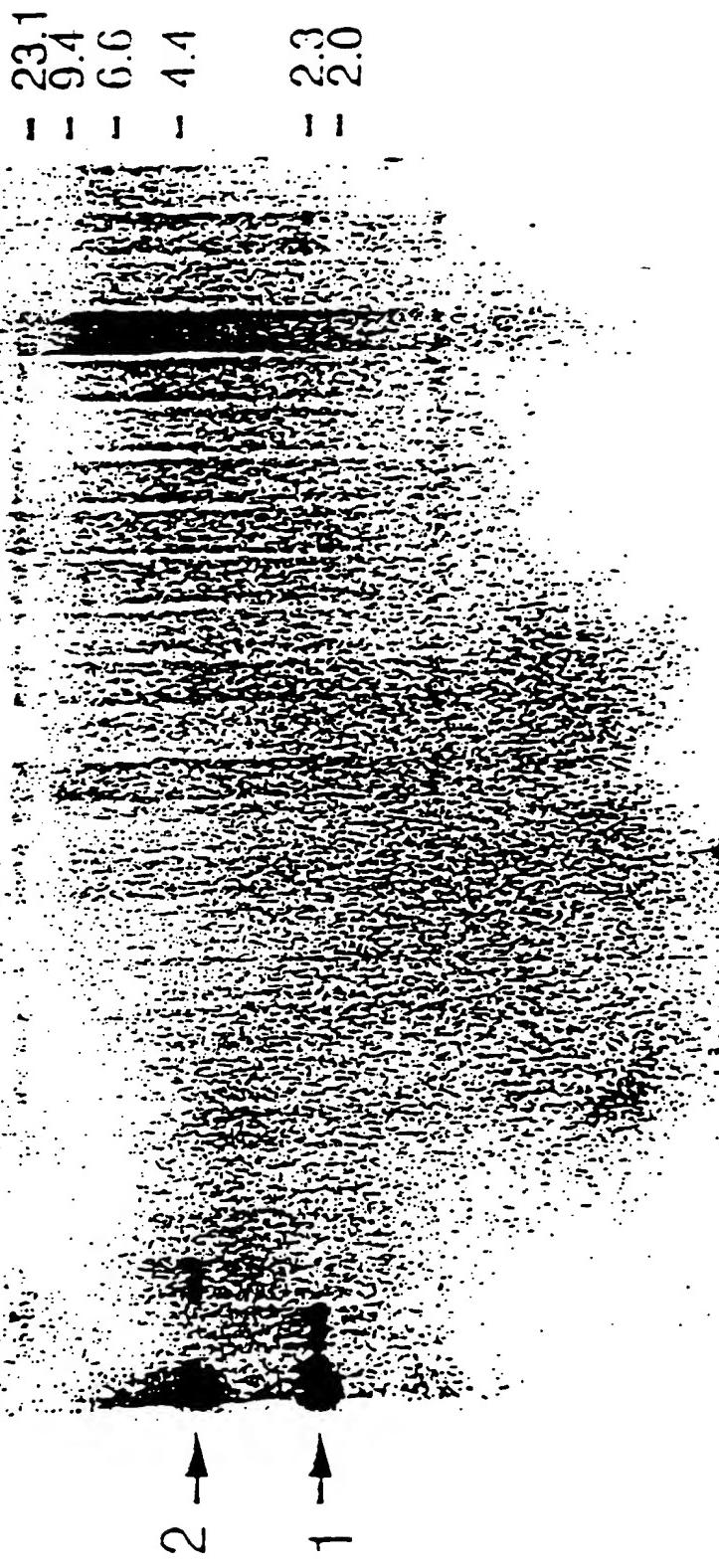
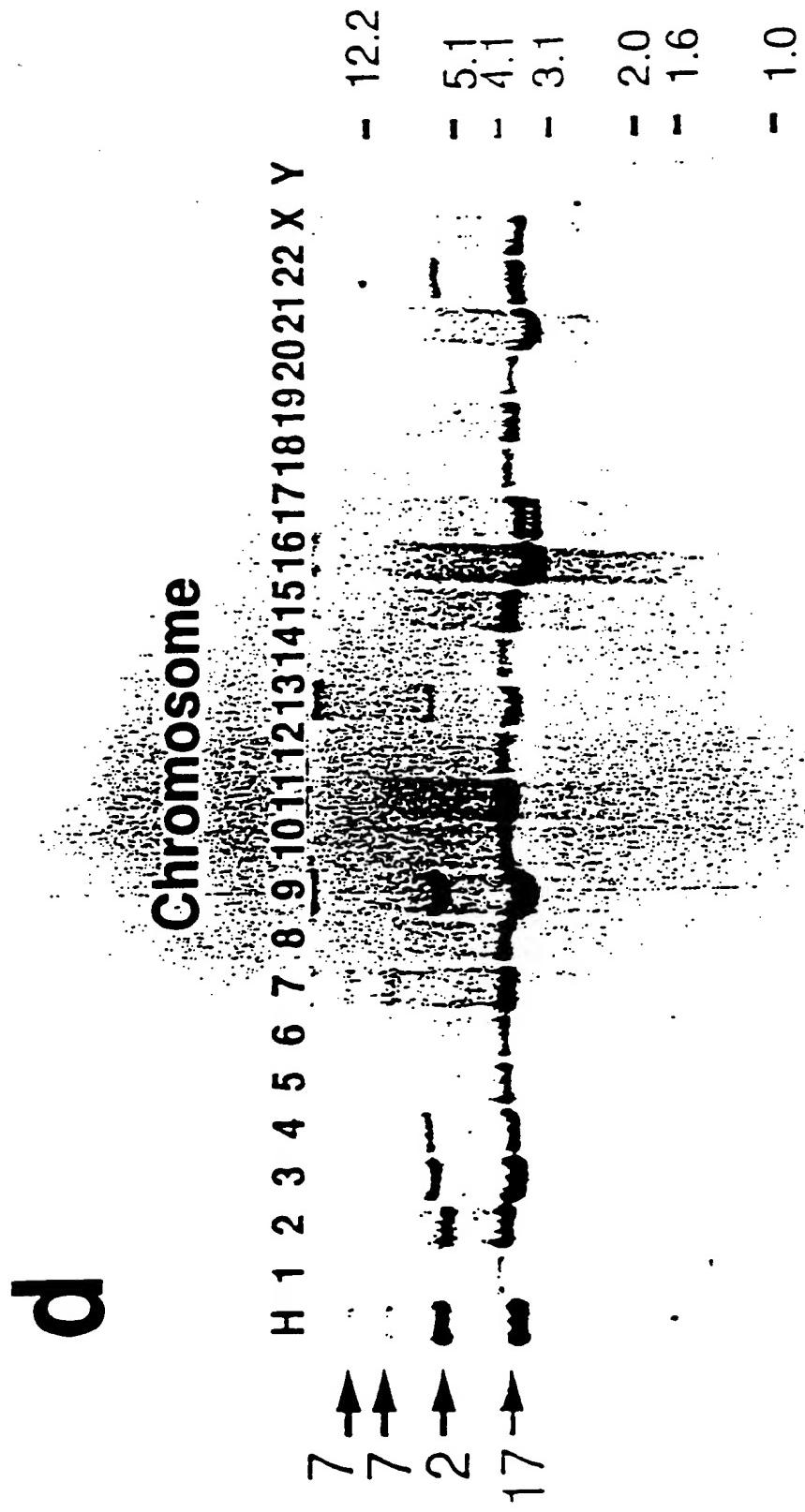


Fig. 19



e

Chromosome

H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

EP 0 679 716 A1

Fig. 20

- 12.2
- 5.1
- 4.1
- 3.1
- 2.0
- 1.6

7,19 ↑
8 ↑
11,12 ↑
11 ↑

Fig. 21

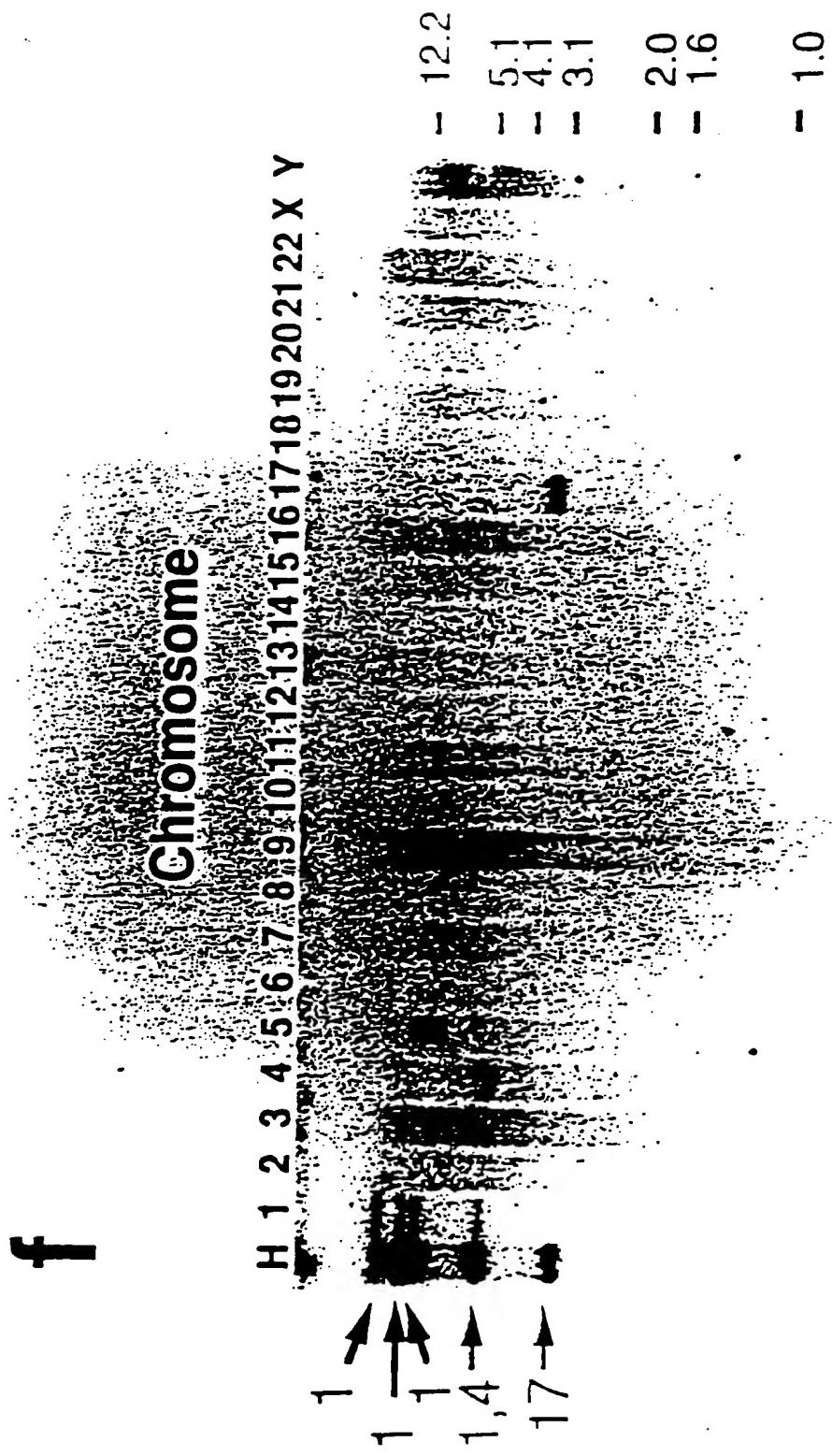


Fig. 22

G
Chromosome



Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Clone	Sequence length	Numbers of bands detected with human whole chromosomes			Chromosomes assigned	Background	
		2/3	2/3; 3/3	3/3		Mouse	Chinese hamster
Single band group:							
c12e11	GS000075	432	1	1	1	1	9
c12e06	GS000062	540	1	1	1	1	6,15
c12g01	GS000290	212	1	1	1	1	3
c13e25	GS000117	359	1	1	1	1	11+
c13e07	GS000120	355	1	1	1	1	2
c13f10	GS000296	267	1	1	1	1	14
c13h01	GS000273	133	1	1	1	1	12+
c13h02	GS000322	167	1	1	1	1	6
d0gG2	GS000095	397	1	1	1	1	3
d0h07	GS000154	313	1	1	1	1	11
d15t0	GS000343	153	1	1	1	1	20
hm01e12	GS000223	246	1	1	1	1	27
hm01e09	GS000423	157	0	1	1	1	1
hm01e12	junk	394	1	1	1	1	17
hm01f05	GS000066	454	1	1	1	1	19,22
hm01f10	GS000299	173	0	1	1	1	10
hm01g09	GS000053	477	1	1	1	1	6
hm01h07	GS000115	363	1	1	1	1	12
hm02a02	GS000130	344	1	1	1	1	4
hm02a04	GS000329	164	1	1	0	1	10
hm02e01	GS000293	271	1	1	1	1	15
hm02e01	GS000015	590	1	1	1	1	20
hmC2e02	GS000342	156	0	1	1	1	14
hm02e05	GS000401	223	1	1	0	1	n.d.
hm02g02	GS000191	278	1	1	1	1	17
hm05e05	GS000251	219	1	1	1	1	6
hm05e10	junk	392	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	1
km20l	junk	169	1	1	1	0	n.d.
s10S	GS000001	703	1	1	1	1	5
s11O	GS000057	471	1	1	1	1	3
s11d11	GS000307	#175	0	0	0	1	7
s11hC1	GS000293	204	1	1	1	1	3
s147	GS000050	461	1	1	1	1	2
s14e06	junk	639	1	1	1	1	0
s14g02	GS000152	322	1	1	1	1	2
s14h12	GS000271	193	1	1	1	1	2
s15O	GS000143	330	1	1	1	1	17
s15G	GS000002	306	1	1	1	1	2
s15B11	GS000250	221	1	1	1	1	14
s179	GS000273	196	1	1	1	1	n.d.
s246	GS000234	241	1	1	1	1	2
s247	GS000147	153	1	1	1	1	0
s270	junk	135	1	1	1	1	0

Fig. 24

Clone	Sequence length	Numbers of bands detected with human whole chromosomes					Chromosomes assigned	Background	
		2	2/3 _a	2/3 _b	3/3 _a	3/3 _b		Chinese Mouse hamster	
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000255	207	1	1	0	1	6,15	1	1
s334	GS000163	312	1	1	1	1	1	0	0
s337	GS000278	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	587	1	1	1	1	2	2	1
s633	GS000166	311	1	1	1	1	22	1	1
s550	GS000041	644	1	1	1	1	12	0	0
cwl-04	GS000025	537	1	1	1	1	3,7	0	0
cwl-19	GS000213	255	1	1	1	1	17	0	0
cwl-32	junk	250	1	1	1	1	5	0	0
cwl-37	GS000237	235	1	1	1	1	22	0	0
cwl-42	junk	391	1	1	1	1	8	1	1
cwl-43	GS000096	178	1	1	1	1	14	0	0
cwl-96	GS000133	339	1	1	1	1	11	0	0
Two band group :									
c12d12	GS000195	277	1	2	2	2	1,	1	1
c13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	5
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000181	292	2	2	2	2	1,2	0	0
hm02a03	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	253	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm03f07	GS000043	503	1	1	2	1	3,	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6,	0	0
s124	GS000083	402	2	2	2	2	9,	1	1
s144	GS000122	342	1	2	2	2	1,7	0	0
s14c03	GS000239	243	1	2	2	2	2,	3	2
s15c02	junk	439	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	284	2	2	2	2	11,	0	0
s234	GS000124	153	2	2	2	2	1,	3	1
s253	GS000235	239	2	2	2	2	11,	0	0
s272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Clone	Sequence length	Numbers of bands detected with human whole chromosomes					Chromosomes assigned	Background	
		S	E/B ₁	E/B ₂	S ₁ /B ₂	Mouse		Mouse	Chinese hamster
s311	GS000092	133	1	1	2	2	16.	1	1
s313	junk	132	2	2	1	0	20.	0	0
s317	GS000100	139	0	0	1	2	14,14	1	1
s336	GS000134	337	2	2	2	2	12,14	0	0
s333	GS00139	233	2	2	2	1	22.X	0	0
s339	GS000233	137	2	1	1	2	17.	0	0
s394	GS000063	449	2	1	2	2	13,14	0	0
s396	junk	277	2	2	2	2	17.	0	1
s455	junk	452	1	2	2	1	4.	0	0
s456	GS000236	132	2	2	2	2	8,10	1	2
s465	GS000201	274	1	1	2	2	6,15	0	0
s633	junk	250	1	1	1	2	9,13	0	0
s639	GS000257	205	1	2	2	2	2X	0	0
s656	GS000025	#590	2	2	0	2	6,11	0	0
tw1-33	junk	352	2	2	2	2	1.	0	0
tw1-39	GS000153	#321	2	2	2	2	17.	0	0
tw1-70	GS000061	441	1	1	2	1	11.	0	0
tw1-80	junk	453	2	2	1	2	9,17	2	2
tw1-87	GS000152	316	2	2	2	2	7.	0	0
Three band group									
d0h06	GS000080	417	3	3	3	1	1.	0	0
hm05b07	junk	336	2	3	3	3	5.	0	0
hm05g02	GS000209	267	2	2	2	1	3,17,19	1	1
s129	GS000107	378	3	3	3	3	n.d.	1	1
s173	GS000357	146	1	2	2	3	2.	0	0
s17a10	GS000294	131	3	3	3	3	2,13,22	1	1
s308	GS000412	638	2	2	2	3	XX	1	1
s401	GS000224	249	2	3	1	3	6,6.	0	0
s654	GS000045	491	3	3	3	3	1,22.	0	0
tw1-82	GS000208	267	3	3	3	3	13.	4	0
Four band group									
c12g07	GS000154	320	4	4	2	3	5, 14.	0	0
c13a08	GS000055	508	3	3	4	4	2,7,7,17	1	2
c13c04	GS000106	#376	4	3	3	3	n.d.	0	2
c13e09	GS000302	193	4	2	4	4	2,17.	7	2
s136	GS000160	315	4	4	4	4	4X.	2	1
s163	GS000004	#618	4	4	4	2	4,4,8,20	3	1
s479	GS000130	293	4	4	2	2	7,8,11,11,12,19	0	0
Group with 5 or more bands									
c12f08	GS000251	217	5	5	5	2	2,7,9,14.	2	0
hc01	junk	374	12	12	13	13	1,2,6.	22	20
hd10	junk	361	4	4	4	8	n.d.	12	6
hc10	junk	173	6	2	3	3	6,3,9,19,21.	3	3
hm01c05	GS000305	176	9	7	5	5	X	9	8
hm01f04	GS000246	215	8	10	5	5	n.d.	12	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14	6

Fig. 26

Numbers of bands detected with human whole chromosomes							Chromosomes assigned		Background	
Clone	Sequence length	5	5/3 ₁	5/3 ₂	5/3 ₃		Mouse	Chinese hamster		
hm02f09	GS000273	442	5	7	7	5	3,3,6,11,13,14,15,16	0	0	
hm05z03	GS000096	373	5	6	4	6	2,3,17,	3	3	
hm05z04	GS000236	#239	6	6	6	7	n.d.	8	5	
km501	junk	350	3	5	5	5	13,	14	7	
s11f06	GS000319	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3	
s14f01	GS000407	252	12	11	10	9	1,6,9,13,	6	3	
s173	GS000094	397	5	4	6	3	1,1,1,1,4,17	0	0	
s251	GS000323	157	10	12	11	14	13,	9	5	
s341	junk	494	9	9	8	6	n.d.	15	3	
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1	
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X,	3	5	
tw1-63	junk	203	3	10	10	12	3,4,	17	11	
Bands not detected:										
el3g02	GS000340	157	0	0	0	0	-	-	-	
hm01e10	junk	232	0	0	0	0	-	-	-	
hm02d11	GS000274	196	0	0	0	0	-	-	-	
s323	GS000273	194	0	0	0	0	-	-	-	
s359	GS000199	279	0	0	0	0	-	-	-	
s511	junk	233	0	0	0	0	-	-	-	
s645	GS000012	#734	0	0	0	0	-	-	-	
s647	GS000195	360	0	0	0	0	-	-	-	
s651	junk	540	0	0	0	0	-	-	-	

INTERNATIONAL SEARCH REPORT

International application No.

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A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
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 Further documents are listed in the continuation of Box C. See patent family annex.^a Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document not published on or after the international filing date

"L" document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, e.g., exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"Δ" document member of the same patent family

Date of the actual completion of the international search February 6, 1995 (06. 02. 95)	Date of mailing of the international search report March 7, 1995 (07. 03. 95)
Name and mailing address of the ISA/ Japanese Patent Office Facsimile No.	Authorized officer Telephone No.

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International application No.

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
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International application No.
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X	J. Clin. Invest., Vol. 83, 1989, Look, A. T. et al. "The human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N" p. 1299-1307	1-6 (1469)
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X	Nucleic Acids Res., Vol. 18, 1990, Liebhaber, S. A. et al. "Characterization of a human cDNA encoding a widely expressed and highly conserved cysteine-rich protein with an unusual zinc-finger motif" p. 3871-3879	1-6 (1642)
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X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
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International application No.

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X	Immunogenetics, Vol. 37, 1993, Emi, N. et al. "Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfamily" p. 193-198	1-6 (2556)
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International application No.
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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	J. Biol. Chem., Vol. 267, 1992, White, R. T. et al. "Human adipsin is identical to complement factor D and expressed at high levels in adipose tissue" p. 9210-9213	1-6 (2802)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Rouault, T. A. et al. "Cloning of the cDNA encoding RNA regulatory protein-the human iron-responsive element-binding protein" p. 7958-7962	1-6 (2832)
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X	Cell, Vol. 58, 1989, Mellentin, J. D. et al. "LYL-1, a novel gene involved by chromosomal translocation in T-cell leukemia, codes for a protein with a helix-loop-helix DNA binding motif" p. 77-83	1-6 (3023)
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X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

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International application No.
PCT/JP94/01916

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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
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X	J. Cell Biol., Vol. 111, 1990, Fishman, G. I. et al. "Molecular Characterization and Functional Expression of the Human Cardiac Gap Junction Channel" p. 589-598	1-6 (3403)
X	Cell, Vol. 40, 1985, Ebina, Y. et al. "The human insulin receptor cDNA: The structural basis for hormone-activated membrane signalling" p. 747-758	1-6 (3447)
X	Oncogene, Vol. 5, 1990, Westin, E. H. et al. "Alternative splicing of the human c-myb gene" p. 1117-1124	1-6 (3529)
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X	Nucleic Acids Res., Vol. 18, 1990, Roessler, B. J. et al. "Cloning of two distinct copies of human phosphoribosyl pyrophosphate synthetase cDNA" p. 193-193	1-6 (3828)

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International application No.

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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biochem., Vol. 109, 1991, Sonoda, T. et. al. "Complete nucleotide sequence of human phosphoribosyl pyrophosphate synthetase subunit I (PRS I) cDNA and a comparison with human and rat PRPS gene families" p. 361-364	1-6 (3828)
X	J. Biol. Chem., Vol. 263, 1988, Wermuth, B. et al. "Human carbonyl reductase: Nucleotide sequence analysis of a cDNA and amino acid sequence of the encoded protein" p. 16185-16188	1-6 (4033)
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Schuetz, T. J. et al. "Isolation of a cDNA for HSF2: Evidence for two heat shock factor genes in humans' p. 6911-6915	1-6 (4093)
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X	J. Biol. Chem., Vol. 268, 1993, David, V. et al. "Interaction with newly synthesized and retained proteins in the endoplasmic reticulum suggests a chaperone function for human integral membrane protein IP90 (calnexin)" p. 9585-9592	1-6 (4373)
X	J. Exp. Med., Vol. 172, 1990, Tekamp-Olson, P. et al. "Cloning and Characterization of cDNAs for Murine Macrophage Inflammatory Protein 2 and its Human Homologues" p. 911-919	1-6 (4452)

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X	J. Biol. Chem., Vol. 267, 1992, Mckenzie, T. L. et al. "Molecular cloning, expression, and characterization of the cDNA for the rat hepataic squalene synthase" p. 21368-21374	1-6 (4818)
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